

1/6

Figure 1

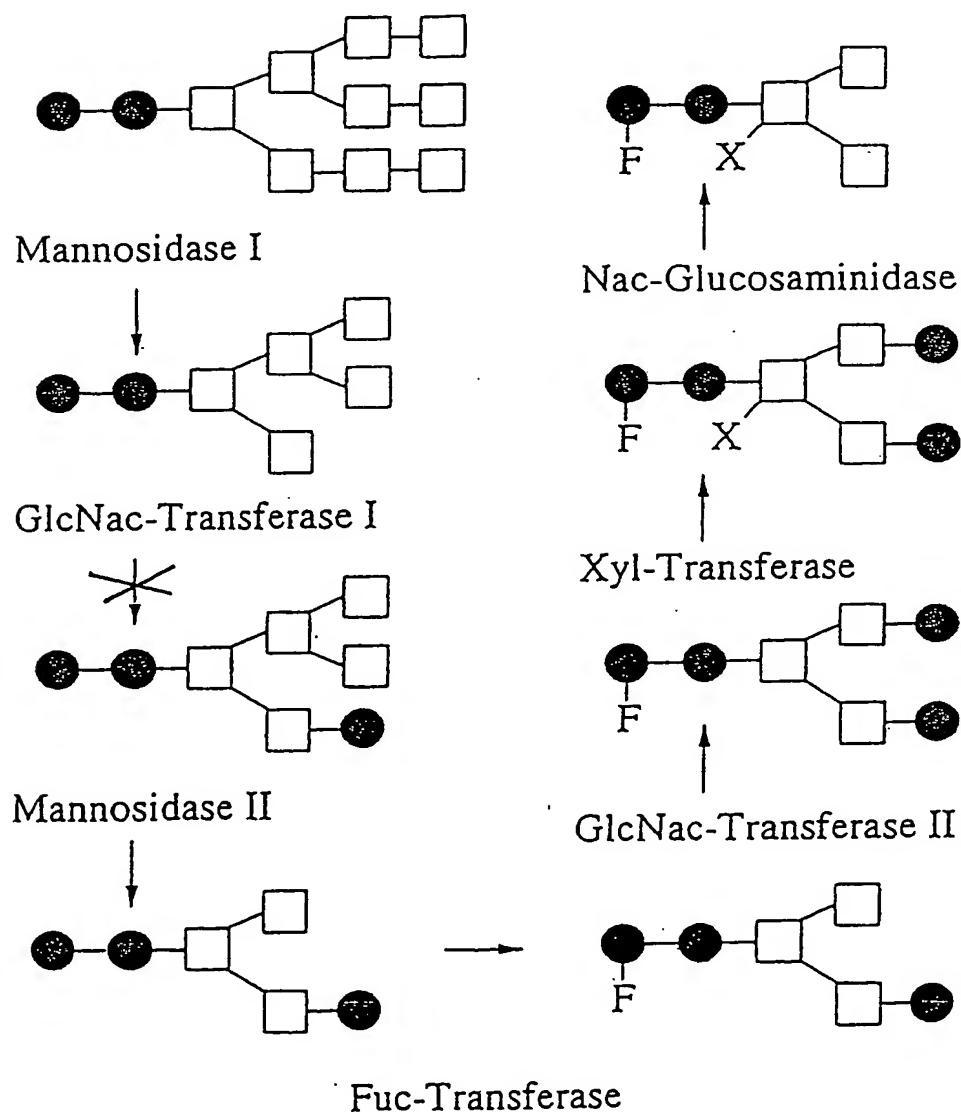


Figure 2

A1 GntI cDNA

GAATTCGCGG CCGCCTGAGA AACCCCTCGAA TTCAATTTTCG CATTTGGCAG AG ATG	55
Met	
1	
AGA GGG AAC AAG TTT TGC TTT GAT TTA CGG TAC CTT CTC GTC GTG GCT	103
Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala	
5 10 15	
GCT CTC GCC TTC ATC TAC ATA CAG ATG CGG CTT TTC GCG ACA CAG TCA	151
Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser	
20 25 30	
GAA TAT GTA GAC CGC CTT GCT GCT GCA ATT GAA GCA GAA AAT CAT TGT	199
Glu Tyr Val Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His Cys	
35 40 45	
ACA AGT CAG ACC AGA TTG CTT ATT GAC AAG ATT AGC CAG CAG CAA GGA	247
Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly	
50 55 60 65	
AGA GTA GTA GCT CTT GAA GAA CAA ATG AAG CAT CAG GAC CAG GAG TGC	295
Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys	
70 75 80	
CGG CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG GGC ATA AAA	343
Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys	
85 90 95	
AAG TTA ATC CGA GAT GTG CAG ATG CCA GTG GCA GCT GTA GTT GTT ATG	391
Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met	
100 105 110	
GCT TGC AGT CGT ACT GAC TAC CTG GAG AGG ACT ATT AAA TCC ATC TTA	439
Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu	
115 120 125	
AAA TAC CAA ACA TCT GTT GCA TCA AAA TAT CCT CTT TTC ATA TCC CAG	487
Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln	
130 135 140 145	
GAT GGA TCA AAT CCT GAT GTA AGA AAG CTT GCT TTG AGC TAT GGT CAG	535
Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln	
150 155 160	
CTG ACG TAT ATG CAG CAC TTG GAT TAT GAA CCT GTG CAT ACT GAA AGA	583
Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg	
165 170 175	
CCA GGG GAA CTG GTT GCA TAC TAC AAG ATT GCA CGT CAT TAC AAG TGG	631
Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp	
180 185 190	
GCA TTG GAT CAG CTG TTT CAC AAG CAT AAT TTT AGC CGT GTT ATC ATA	679
Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile	
195 200 205	
CTA GAA GAT GAT ATG GAA ATT GCT GCT GAT TTT TTT GAC TAT TTT CAG	727
Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu	
210 215 220 225	

Figure 2 (continued)

GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG <u>GCT ATT TCT</u>	775
Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser.	
230 235 240	
<u>TCT TGG AAT GAC AAT GGA CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT</u>	823
Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala	
245 250 255	
CTT TAC CGC TCA <u>GAC TTT TTT CCT GGT CTT GGA TGG</u> ATG CTT TCA AAA	871
Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys	
260 265 270	
TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT	919
Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp	
275 280 285	
GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC	967
Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg	
290 295 300 305	
CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG	1015
Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu	
310 315 320	
GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC	1063
Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val	
325 330 335	
CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC	1111
Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn	
340 345 350	
TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC	1159
Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His	
355 360 365	
GGA GCT GAT GCT GTT TTG AAA GCA TTT AAC ATA GAT GGT GAT GTG CGT	1207
Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg	
370 375 380 385	
ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT	1255
Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe	
390 395 400	
GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA	1303
Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys	
405 410 415	
GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT	1351
Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val	
420 425 430	
TCC CCT GAT TCT CTT CGA CAA CTT GGA GTT GAA GAT ACT TAG	1393
Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr End	
435 440 445	
CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA	1453
GAGCTGACAC GAAAAGTATG ACTACCAGTA GCTACATGCA ACATTTTAAT GTTAATGGAA	1513
GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT	1573
ACAAACATAA AGAGGAAATG TTGCCCTATA AAAACAAATT TTTTGTTTCT AAGAAGGAAC	1633
GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC	1669

4/6

Figure 3A

Hu	Ra	Mo	Ce	
35 (59)	36 (57)	35 (59)	33 (57)	St
	92 (95)	91 (94)	38 (57)	Hu
		90 (93)	38 (57)	Ra
			38 (58)	Mo

Figure 3B

A_Stb-A1	1	MRGNKFCFDLRYLLAAAFIYIQMRLEATQSEYVDRLAAAIEAENHCT
B_Ntb-A9	1	MRGNKECCDERYLLIAAFIYIQMRLEATQSEYADR LAAAE AENHCT
C_Atb-Full	1	..MAFISCDLRELLIPAAFMFIYIQMRLEATQSYADRLESAIESENHCT
A_Stb-A1	51	SQTRLLIDKISQOQGRIVALEEQMKQDOECROLRALVODLESKGIKKLI
B_Ntb-A9	51	SQTRLLIDKISQOQGRIVALEEQMKRODOECROLRALVODLESKGIKKLI
C_Atb-Full	49	SOMRGLIDKISQOSRIVALEEMKNRODELVOLKDLQOTFEKKGIKKLI
A_Stb-A1	101	GPVOMPVAADVVMACSRDYLERTIKSILKYQTSVASKYPLFISODGSP
B_Ntb-A9	101	GPVOMPVAADVVMACNRADYLETILKSILKYQTSVASKYPLFISODGSEP
C_Atb-Full	99	QGGOMPVAADVVMACSRADYLERTKSLTYOTFVASKYPLFISODGSIQ
A_Stb-A1	151	DVRKLALSYGOLTYMOHLDEP VHTERPGELTAYYKIARHYKWALDOLF
B_Ntb-A9	151	DVRKLALSYGOLTYMOHLDFEP VHTERPGELTAYYKIARHYKWALDOLFY
C_Atb-Full	149	AVNSKLSYGO LTYMOHLDFEPV VTERPGELTAYYKIARHYKWALDOLF
A_Stb-A1	201	KHNFSRVIILEDDMEIAADFFDYFEAGATLLDRDKSIMAISSWNDNGOMQ
B_Ntb-A9	201	KHNFSRVIILEDDMEIAPDFFDYFEAGATLLDRDKSIMAISSWNDNGOMQ
C_Atb-Full	199	KHKFSRVIILEDDMEIAPDFFDYFEAGATLLDRDKSIMAISSWNDNGOMQ
A_Stb-A1	251	EVQDPDALYRSDFFPGLGWMLSKSTWSELSPKWPKAYWDDWLRLKENHRG
B_Ntb-A9	251	EVQDPYALYRSDFFPGLGWMLSKSTWDELSPKWPKAYWDDWLRLKENHRG
C_Atb-Full	249	FVEDPYALYRSDFFPGLGWMLKSTWDELSPKWPKAYWDDWLRLKENHKG
A_Stb-A1	301	ROFIRPEVCRTYNFGEHGSSLGQFFKQYLEPIKLNDVQVDWKSMDLSYLL
B_Ntb-A9	301	ROFIRPEVCRTYNFGEHGSSLGQFFKQYLEPIKLNDVQVDWKSMDLSYLL
C_Atb-Full	299	ROFIAPVCRTYNFGEHGSSLGQFFSOYLEPIKLNDVTVDWKEKDLGYLT
A_Stb-A1	351	EDNYVKHEGDLVKKAKPIHGADAVLKAFNIDGDVRIQYRDQDFFENIARQ
B_Ntb-A9	351	EDNYVKHEGDLVKKAKPIHGADAVLKAFNIDGDVRIQYRDQDFFENIARQ
C_Atb-Full	349	EGNYTKYFSGLVQANPIQGSGLVLKAQNIKDDDRIRYKQDFFERIAGP
A_Stb-A1	401	EGIFEEWKDGVPRAAAYKGIVVERQTSRRVFLVSPDSLRQLGIEDT
B_Ntb-A9	401	EGIFEEWKDGVPRAAAYKGIVVERQTSRRVFLVGSLSLOQLGIEDT
C_Atb-Full	399	EGIFEEWKDGVPRAAAYKGIVVERQTSRRVFLVGPDSLMOLGIRMS

Figure 4

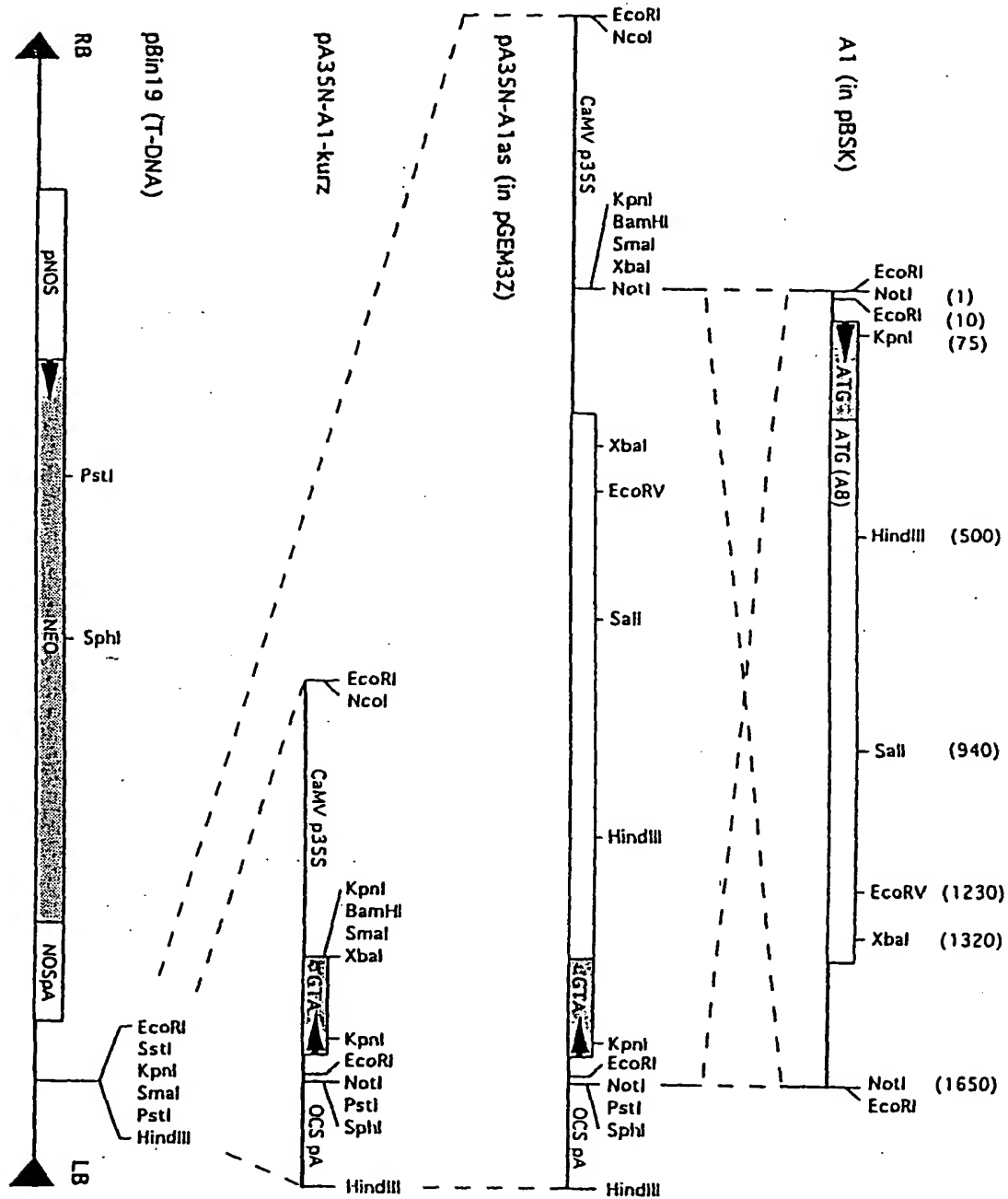


Figure 5

6/6

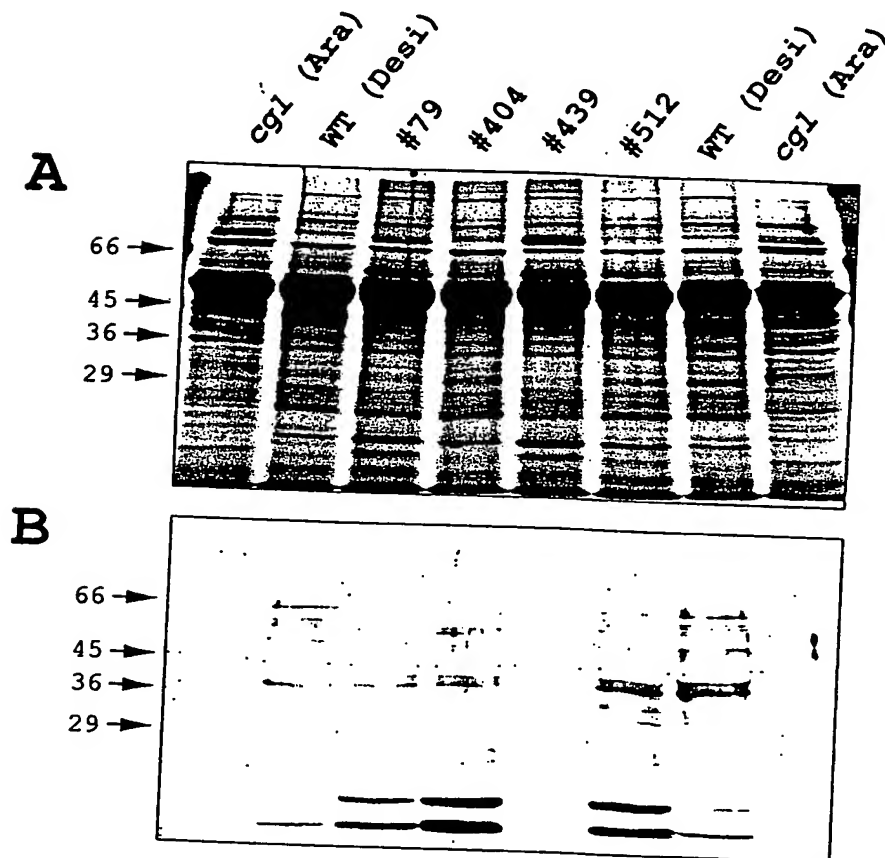
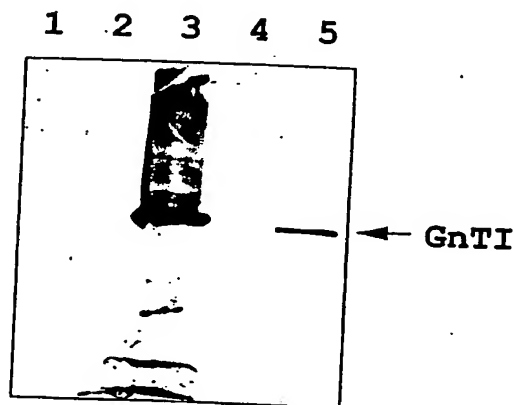


Figure 6



BEST AVAILABLE COPY